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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/024,369

DATE: 01/15/2002  
 TIME: 18:07:07

Input Set : A:\RTS-0353 Sequence Listing.txt  
 Output Set: N:\CRF3\01152002\J024369.raw

**ENTERED**

6 <110> APPLICANT: Alexander H. Borchers  
 7 Donna T. Ward  
 8 Susan M. Freier  
 10 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF ABC TRANSPORTER MHC 1 EXPRESSION  
 12 <130> FILE REFERENCE: RTS-0353  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/024,369  
 C--> 14 <141> CURRENT FILING DATE: 2001-12-17  
 14 <160> NUMBER OF SEQ ID NOS: 91  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 20  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: Artificial Sequence  
 22 <220> FEATURE:  
 24 <223> OTHER INFORMATION: Antisense Oligonucleotide  
 26 <400> SEQUENCE: 1  
 27 tccgtcatcg ctcctcaggg 20  
 30 <210> SEQ ID NO: 2  
 31 <211> LENGTH: 20  
 32 <212> TYPE: DNA  
 33 <213> ORGANISM: Artificial Sequence  
 35 <220> FEATURE:  
 37 <223> OTHER INFORMATION: Antisense Oligonucleotide  
 39 <400> SEQUENCE: 2  
 40 atgcattctg cccccaagga 20  
 43 <210> SEQ ID NO: 3  
 44 <211> LENGTH: 2247  
 45 <212> TYPE: DNA  
 46 <213> ORGANISM: Homo sapiens  
 48 <220> FEATURE:  
 50 <221> NAME/KEY: CDS  
 51 <222> LOCATION: (1)...(2247)  
 53 <400> SEQUENCE: 3  
 54 atg gct agc tct agg tgt ccc gct ccc cgc ggg tgc cgc tgc ctc ccc 48  
 55 Met Ala Ser Ser Arg Cys Pro Ala Pro Arg Gly Cys Arg Cys Leu Pro  
 56 1 5 10 15  
 57 gga gct tct ctc gca tgg ctg ggg aca gta ctg cta ctt ctc gcc gac 96  
 58 Gly Ala Ser Leu Ala Trp Leu Gly Thr Val Leu Leu Leu Leu Ala Asp  
 59 20 25 30  
 60 tgg gtg ctg ctc cgg acc gcg ctg ccc cgc ata ttc tcc ctg ctg gtg 144  
 61 Trp Val Leu Leu Arg Thr Ala Leu Pro Arg Ile Phe Ser Leu Leu Val  
 62 35 40 45  
 63 ccc acc gcg ctg cca ctg ctc cgg gtc tgg gcg gtg ggc ctg agc cgc 192  
 64 Pro Thr Ala Leu Pro Leu Leu Arg Val Trp Ala Val Gly Leu Ser Arg  
 65 50 55 60  
 66 tgg gcc gtg ctc tgg ctg ggg gcc tgc ggg gtc ctc agg gca acg gtt 240  
 67 Trp Ala Val Leu Trp Leu Gly Ala Cys Gly Val Leu Arg Ala Thr Val  
 68 65 70 75 80

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69 ggc tcc aag agc gaa aac gca ggt gcc cag ggc tgg ctg gct gct ttg      288
70 Gly Ser Lys Ser Glu Asn Ala Gly Ala Gln Gly Trp Leu Ala Ala Leu
71                               85                               90                               95
72 aag cca tta gct gcg gca ctg ggc ttg gcc ctg ccg gga ctt gcc ttg      336
73 Lys Pro Leu Ala Ala Ala Leu Gly Leu Ala Leu Pro Gly Leu Ala Leu
74                               100                               105                               110
75 ttc cga gag ctg atc tca tgg gga gcc ccc ggg tcc gcg gat agc acc      384
76 Phe Arg Glu Leu Ile Ser Trp Gly Ala Pro Gly Ser Ala Asp Ser Thr
77                               115                               120                               125
78 agg cta ctg cac tgg gga agt cac cct acc gcc ttc gtt gtc agt tat      432
79 Arg Leu Leu His Trp Gly Ser His Pro Thr Ala Phe Val Val Ser Tyr
80                               130                               135                               140
81 gca gcg gca ctg ccc gca gca gcc ctg tgg cac aaa ctc ggg agc ctc      480
82 Ala Ala Ala Leu Pro Ala Ala Ala Leu Trp His Lys Leu Gly Ser Leu
83 145                               150                               155                               160
84 tgg gtg ccc ggc ggt cag ggc ggc tct gga aac cct gtg cgt cgg ctt      528
85 Trp Val Pro Gly Gly Gln Gly Gly Ser Gly Asn Pro Val Arg Arg Leu
86                               165                               170                               175
87 cta ggc tgc ctg ggc tcg gag acg cgc cgc ctc tcg ctg ttc ctg gtc      576
88 Leu Gly Cys Leu Gly Ser Glu Thr Arg Arg Leu Ser Leu Phe Leu Val
89                               180                               185                               190
90 ctg gtg gtc ctc tcc tct ctt ggg gag atg gcc att cca ttc ttt acg      624
91 Leu Val Val Leu Ser Ser Leu Gly Glu Met Ala Ile Pro Phe Phe Thr
92                               195                               200                               205
93 ggc cgc ctc act gac tgg att cta caa gat ggc tca gcc gat acc ttc      672
94 Gly Arg Leu Thr Asp Trp Ile Leu Gln Asp Gly Ser Ala Asp Thr Phe
95                               210                               215                               220
96 act cga aac tta act ctc atg tcc att ctc acc ata gcc agt gca gtg      720
97 Thr Arg Asn Leu Thr Leu Met Ser Ile Leu Thr Ile Ala Ser Ala Val
98 225                               230                               235                               240
99 ctg gag ttc gtg ggt gac ggg atc tat aac aac acc atg ggc cac gtg      768
100 Leu Glu Phe Val Gly Asp Gly Ile Tyr Asn Asn Thr Met Gly His Val
101                               245                               250                               255
102 cac agc cac ttg cag gga gag gtg ttt ggg gct gtc ctg cgc cag gag      816
103 His Ser His Leu Gln Gly Glu Val Phe Gly Ala Val Leu Arg Gln Glu
104                               260                               265                               270
105 acg gag ttt ttc caa cag aac cag aca ggt aac atc atg tct cgg gta      864
106 Thr Glu Phe Phe Gln Gln Asn Gln Thr Gly Asn Ile Met Ser Arg Val
107                               275                               280                               285
108 aca gag gac acg tcc acc ctg agt gat tct ctg agt gag aat ctg agc      912
109 Thr Glu Asp Thr Ser Thr Leu Ser Asp Ser Leu Ser Glu Asn Leu Ser
110                               290                               295                               300
111 tta ttt ctg tgg tac ctg gtg cga ggc cta tgt ctc ttg ggg atc atg      960
112 Leu Phe Leu Trp Tyr Leu Val Arg Gly Leu Cys Leu Leu Gly Ile Met
113 305                               310                               315                               320
114 ctc tgg gga tca gtg tcc ctc acc atg gtc acc ctg atc acc ctg cct      1008
115 Leu Trp Gly Ser Val Ser Leu Thr Met Val Thr Leu Ile Thr Leu Pro
116                               325                               330                               335
117 ctg ctt ttc ctt ctg ccc aag aag gtg gga aaa tgg tac cag ttg ctg      1056

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118	Leu	Leu	Phe	Leu	Leu	Pro	Lys	Lys	Val	Gly	Lys	Trp	Tyr	Gln	Leu	Leu	
119				340					345					350			
120	gaa	gtg	cag	gtg	cgg	gaa	tct	ctg	gca	aag	tcc	agc	cag	gtg	gcc	att	1104
121	Glu	Val	Gln	Val	Arg	Glu	Ser	Leu	Ala	Lys	Ser	Ser	Gln	Val	Ala	Ile	
122			355					360					365				
123	gag	gct	ctg	tcg	gcc	atg	cct	aca	gtt	cga	agc	ttt	gcc	aac	gag	gag	1152
124	Glu	Ala	Leu	Ser	Ala	Met	Pro	Thr	Val	Arg	Ser	Phe	Ala	Asn	Glu	Glu	
125		370					375					380					
126	ggc	gaa	gcc	cag	aag	ttt	agg	gaa	aag	ctg	caa	gaa	ata	aag	aca	ctc	1200
127	Gly	Glu	Ala	Gln	Lys	Phe	Arg	Glu	Lys	Leu	Gln	Glu	Ile	Lys	Thr	Leu	
128	385					390				395						400	
129	aac	cag	aag	gag	gct	gtg	gcc	tat	gca	gtc	aac	tcc	tgg	acc	act	agt	1248
130	Asn	Gln	Lys	Glu	Ala	Val	Ala	Tyr	Ala	Val	Asn	Ser	Trp	Thr	Thr	Ser	
131				405					410					415			
132	att	tca	ggt	atg	ctg	ctg	aaa	gtg	gga	atc	ctc	tac	att	ggt	ggg	cag	1296
133	Ile	Ser	Gly	Met	Leu	Leu	Lys	Val	Gly	Ile	Leu	Tyr	Ile	Gly	Gly	Gln	
134			420					425					430				
135	ctg	gtg	acc	agt	ggg	gct	gta	agc	agt	ggg	aac	ctt	gtc	aca	ttt	gtt	1344
136	Leu	Val	Thr	Ser	Gly	Ala	Val	Ser	Ser	Gly	Asn	Leu	Val	Thr	Phe	Val	
137		435					440					445					
138	ctc	tac	cag	atg	cag	ttc	acc	cag	gct	gtg	gag	gta	ctg	ctc	tcc	atc	1392
139	Leu	Tyr	Gln	Met	Gln	Phe	Thr	Gln	Ala	Val	Glu	Val	Leu	Leu	Ser	Ile	
140		450				455				460							
141	tac	ccc	aga	gta	cag	aag	gct	gtg	ggc	tcc	tca	gag	aaa	ata	ttt	gag	1440
142	Tyr	Pro	Arg	Val	Gln	Lys	Ala	Val	Gly	Ser	Ser	Glu	Lys	Ile	Phe	Glu	
143	465				470				475							480	
144	tac	ctg	gac	cgc	acc	cct	cgc	tgc	cca	ccc	agt	ggt	ctg	ttg	act	ccc	1488
145	Tyr	Leu	Asp	Arg	Thr	Pro	Arg	Cys	Pro	Pro	Ser	Gly	Leu	Leu	Thr	Pro	
146			485					490				495					
147	tta	cac	ttg	gag	ggc	ctt	gtc	cag	ttc	caa	gat	gtc	tcc	ttt	gcc	tac	1536
148	Leu	His	Leu	Glu	Gly	Leu	Val	Gln	Phe	Gln	Asp	Val	Ser	Phe	Ala	Tyr	
149			500					505				510					
150	cca	aac	cgc	cca	gat	gtc	tta	gtg	cta	cag	ggg	ctg	aca	ttc	acc	cta	1584
151	Pro	Asn	Arg	Pro	Asp	Val	Leu	Val	Leu	Gln	Gly	Leu	Thr	Phe	Thr	Leu	
152		515					520					525					
153	cgc	cct	ggc	gag	gtg	acg	gcg	ctg	gtg	gga	ccc	aat	ggg	tct	ggg	aag	1632
154	Arg	Pro	Gly	Glu	Val	Thr	Ala	Leu	Val	Gly	Pro	Asn	Gly	Ser	Gly	Lys	
155		530					535					540					
156	agc	aca	gtg	gct	gcc	ctg	ctg	cag	aat	ctg	tac	cag	ccc	acc	ggg	gga	1680
157	Ser	Thr	Val	Ala	Ala	Leu	Leu	Gln	Asn	Leu	Tyr	Gln	Pro	Thr	Gly	Gly	
158	545				550					555						560	
159	cag	ctg	ctg	ttg	gat	ggg	aag	ccc	ctt	ccc	caa	tat	gag	cac	cgc	tac	1728
160	Gln	Leu	Leu	Leu	Asp	Gly	Lys	Pro	Leu	Pro	Gln	Tyr	Glu	His	Arg	Tyr	
161			565					570				575					
162	ctg	cac	agg	cag	gtg	gct	gca	gtg	gga	caa	gag	cca	cag	gta	ttt	gga	1776
163	Leu	His	Arg	Gln	Val	Ala	Ala	Val	Gly	Gln	Glu	Pro	Gln	Val	Phe	Gly	
164			580					585				590					
165	aga	agt	ctt	caa	gaa	aat	att	gcc	tat	ggc	ctg	acc	cag	aag	cca	act	1824
166	Arg	Ser	Leu	Gln	Glu	Asn	Ile	Ala	Tyr	Gly	Leu	Thr	Gln	Lys	Pro	Thr	

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167          595          600          605
168 atg gag gaa atc aca gct gct gca gta aag tct ggg gcc cat agt ttc      1872
169 Met Glu Glu Ile Thr Ala Ala Val Lys Ser Gly Ala His Ser Phe
170          610          615          620
171 atc tct gga ctc cct cag ggc tat gac aca gag gta gac gag gct ggg      1920
172 Ile Ser Gly Leu Pro Gln Gly Tyr Asp Thr Glu Val Asp Glu Ala Gly
173 625          630          635          640
174 agc cag ctg tca ggg ggt cag cga cag gca gtg gcg ttg gcc cga gca      1968
175 Ser Gln Leu Ser Gly Gly Gln Arg Gln Ala Val Ala Leu Ala Arg Ala
176          645          650          655
177 ttg atc cgg aaa ccg tgt gta ctt atc ctg gat gat gcc acc agt gcc      2016
178 Leu Ile Arg Lys Pro Cys Val Leu Ile Leu Asp Asp Ala Thr Ser Ala
179          660          665          670
180 ctg gat gca aac agc cag tta cag gtg gag cag ctc ctg tac gaa agc      2064
181 Leu Asp Ala Asn Ser Gln Leu Gln Val Glu Gln Leu Leu Tyr Glu Ser
182          675          680          685
183 cct gag cgg tac tcc cgc tca gtg ctt ctc atc acc cag cac ctc agc      2112
184 Pro Glu Arg Tyr Ser Arg Ser Val Leu Leu Ile Thr Gln His Leu Ser
185          690          695          700
186 ctg gtg gag cag gct gac cac atc ctc ttt ctg gaa gga ggc gct atc      2160
187 Leu Val Glu Gln Ala Asp His Ile Leu Phe Leu Glu Gly Gly Ala Ile
188 705          710          715          720
189 cgg gag ggg gga acc cac cag cag ctc atg gag aaa aag ggg tgc tac      2208
190 Arg Glu Gly Gly Thr His Gln Gln Leu Met Glu Lys Lys Gly Cys Tyr
191          725          730          735
192 tgg gcc atg gtg cag gct cct gca gat gct cca gaa tga      2247
193 Trp Ala Met Val Gln Ala Pro Ala Asp Ala Pro Glu
194          740          745
197 <210> SEQ ID NO: 4
198 <211> LENGTH: 23
199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
204 <223> OTHER INFORMATION: PCR Primer
206 <400> SEQUENCE: 4
207 tgggtgacgg gatctataac aac      23
210 <210> SEQ ID NO: 5
211 <211> LENGTH: 20
212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
217 <223> OTHER INFORMATION: PCR Primer
219 <400> SEQUENCE: 5
220 ccaaacacct ctccctgcaa      20
223 <210> SEQ ID NO: 6
224 <211> LENGTH: 20
225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:

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230 <223> OTHER INFORMATION: PCR Probe
232 <400> SEQUENCE: 6
233 catgggccac gtgcacagcc                                20
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237 <211> LENGTH: 19
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
243 <223> OTHER INFORMATION: PCR Primer
245 <400> SEQUENCE: 7
246 gaaggtgaag gtcggagtc                                19
249 <210> SEQ ID NO: 8
250 <211> LENGTH: 20
251 <212> TYPE: DNA
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
256 <223> OTHER INFORMATION: PCR Primer
258 <400> SEQUENCE: 8
259 gaagatggtg atgggatttc                                20
262 <210> SEQ ID NO: 9
263 <211> LENGTH: 20
264 <212> TYPE: DNA
265 <213> ORGANISM: Artificial Sequence
267 <220> FEATURE:
269 <223> OTHER INFORMATION: PCR Probe
271 <400> SEQUENCE: 9
272 caagcttccc gttctcagcc                                20
275 <210> SEQ ID NO: 10
276 <211> LENGTH: 20
277 <212> TYPE: DNA
278 <213> ORGANISM: Artificial Sequence
280 <220> FEATURE:
282 <223> OTHER INFORMATION: Antisense Oligonucleotide
284 <400> SEQUENCE: 10
285 ggacacctag agctagccat                                20
288 <210> SEQ ID NO: 11
289 <211> LENGTH: 20
290 <212> TYPE: DNA
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
295 <223> OTHER INFORMATION: Antisense Oligonucleotide
297 <400> SEQUENCE: 11
298 agccatgcga gagaagctcc                                20
301 <210> SEQ ID NO: 12
302 <211> LENGTH: 20
303 <212> TYPE: DNA
304 <213> ORGANISM: Artificial Sequence
306 <220> FEATURE:
308 <223> OTHER INFORMATION: Antisense Oligonucleotide

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/024,369

DATE: 01/15/2002

TIME: 18:07:08

Input Set : A:\RTS-0353 Sequence Listing.txt

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date